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<110>  LANGENFELD, John
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 LeBeau,M.M., Harland,R.M. and Yancopoulos,G.D.  
 <302> Identification of mammalian noggin and its expression in the adult nervous  
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 <303> J. Neurosci.  
 <304> 15  
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 <301> Brunet,L.J., McMahon,J.A., McMahon,A.P. and Harland,R.M.  
 <302> Noggin, cartilage morphogenesis, and joint formation in the mammalian skeleton  
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 <304> 280  
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 <302> Heterozygous mutations in the gene encoding noggin affect human joint morphogenesis  
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Ile Pro Pro Pro Asp Lys Ala Gln His Asn Asp Ser Glu Gln Thr Gln  
 35 40 45

Ser Pro Gln Gln Pro Gly Ser Arg Asn Arg Gly Arg Gly Gln Gly Arg  
 50 55 60

Gly Thr Ala Met Pro Gly Glu Glu Val Leu Glu Ser Ser Gln Glu Ala  
 65 70 75 80



Leu His Val Thr Glu Arg Lys Tyr Leu Lys Arg Asp Trp Cys Lys Thr  
85 90 95

Gln Pro Leu Lys Gln Thr Ile His Glu Glu Gly Cys Asn Ser Arg Thr  
100 105 110

Ile Ile Asn Arg Phe Cys Tyr Gly Gln Cys Asn Ser Phe Tyr Ile Pro  
115 120 125

Arg His Ile Arg Lys Glu Glu Gly Ser Phe Gln Ser Cys Ser Phe Cys  
130 135 140

Lys Pro Lys Lys Phe Thr Thr Met Met Val Thr Leu Asn Cys Pro Glu  
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Arg Cys Ile Ser Ile Asp Leu Asp  
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<301> Lah, M., Brodnicki, T., Maccarone, P., Nash, A., Stanley, E., and Harvey, R.P.

<302> Human cerberus related gene CER1 maps to chromosome 9

<303> Genomics

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<307> 1999

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1				5					10					15		

acc	aca	cgg	cac	cag	gat	ggc	cgc	cag	aat	cag	agt	tct	ctt	tcc	ccc	96
Thr	Thr	Arg	His	Gln	Asp	Gly	Arg	Gln	Asn	Gln	Ser	Ser	Leu	Ser	Pro	
			20					25					30			

gta	ctc	ctg	cca	agg	aat	caa	aga	gag	ctt	ccc	aca	ggc	aac	cat	gag	144
Val	Leu	Leu	Pro	Arg	Asn	Gln	Arg	Glu	Leu	Pro	Thr	Gly	Asn	His	Glu	
			35				40					45				

gaa	gct	gag	gag	aag	cca	gat	ctg	ttt	gtc	gca	gtg	cca	cac	ctt	gta	192
Glu	Ala	Glu	Glu	Lys	Pro	Asp	Leu	Phe	Val	Ala	Val	Pro	His	Leu	Val	
	50					55					60					

gcc	acc	agc	cct	gca	ggg	gaa	ggc	cag	agg	cag	aga	gag	aag	atg	ctg	240
Ala	Thr	Ser	Pro	Ala	Gly	Glu	Gly	Gln	Arg	Gln	Arg	Glu	Lys	Met	Leu	
65					70				75					80		

tcc	aga	ttt	ggc	agg	ttc	tgg	aag	aag	cct	gag	aga	gaa	atg	cat	cca	288
Ser	Arg	Phe	Gly	Arg	Phe	Trp	Lys	Lys	Pro	Glu	Arg	Glu	Met	His	Pro	
			85						90					95		

tcc	agg	gac	tca	gat	agt	gag	ccc	ttc	cca	cct	ggg	acc	cag	tcc	ctc	336
Ser	Arg	Asp	Ser	Asp	Ser	Glu	Pro	Phe	Pro	Pro	Gly	Thr	Gln	Ser	Leu	
			100					105					110			

atc	cag	ccg	ata	gat	gga	atg	aaa	atg	gag	aaa	tct	cct	ctt	cgg	gaa	384
Ile	Gln	Pro	Ile	Asp	Gly	Met	Lys	Met	Glu	Lys	Ser	Pro	Leu	Arg	Glu	
		115				120						125				

gaa	gcc	aag	aaa	ttc	tgg	cac	cac	ttc	atg	ttc	aga	aaa	act	ccg	gct	432
Glu	Ala	Lys	Lys	Phe	Trp	His	His	Phe	Met	Phe	Arg	Lys	Thr	Pro	Ala	
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tct	cag	ggg	gtc	atc	ttg	ccc	atc	aaa	agc	cat	gaa	gta	cat	tgg	gag	480
Ser	Gln	Gly	Val	Ile	Leu	Pro	Ile	Lys	Ser	His	Glu	Val	His	Trp	Glu	

20445-01102

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acc tgc agg aca gtg ccc ttc agc cag act ata acc cac gaa ggc tgt				528
Thr Cys Arg Thr	Val Pro Phe Ser Gln Thr	Ile Thr His Glu Gly Cys		
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Glu Lys Val Val Val	Gln Asn Asn Leu Cys Phe Gly Lys Cys Gly Ser			
	180	185	190	
gtt cat ttt cct gga gcc gcg cag cac tcc cat acc tcc tgc tct cac				624
Val His Phe Pro Gly Ala Ala Gln His Ser His Thr Ser Cys Ser His				
	195	200	205	
tgt ttg cct gcc aag ttc acc acg atg cac ttg cca ctg aac tgc act				672
Cys Leu Pro Ala Lys Phe Thr Thr Met His Leu Pro Leu Asn Cys Thr				
	210	215	220	
gaa ctt tcc tcc gtg atc aag gtg gtg atg ctg gtg gag gag tgc cag				720
Glu Leu Ser Ser Val Ile Lys Val Val Met Leu Val Glu Glu Cys Gln				
	225	230	235	240
tgc aag gtg aag acg gag cat gaa gat gga cac atc cta cat gct ggc				768
Cys Lys Val Lys Thr Glu His Glu Asp Gly His Ile Leu His Ala Gly				
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Glu Ala Glu Glu Lys Pro Asp Leu Phe Val Ala Val Pro His Leu Val  
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Ala Thr Ser Pro Ala Gly Glu Gly Gln Arg Gln Arg Glu Lys Met Leu  
65 70 75 80

Ser Arg Phe Gly Arg Phe Trp Lys Lys Pro Glu Arg Glu Met His Pro  
85 90 95

Ser Arg Asp Ser Asp Ser Glu Pro Phe Pro Pro Gly Thr Gln Ser Leu  
100 105 110

Ile Gln Pro Ile Asp Gly Met Lys Met Glu Lys Ser Pro Leu Arg Glu  
115 120 125

Glu Ala Lys Lys Phe Trp His His Phe Met Phe Arg Lys Thr Pro Ala  
130 135 140

Ser Gln Gly Val Ile Leu Pro Ile Lys Ser His Glu Val His Trp Glu  
145 150 155 160

Thr Cys Arg Thr Val Pro Phe Ser Gln Thr Ile Thr His Glu Gly Cys  
165 170 175

Glu Lys Val Val Val Gln Asn Asn Leu Cys Phe Gly Lys Cys Gly Ser  
180 185 190

Val His Phe Pro Gly Ala Ala Gln His Ser His Thr Ser Cys Ser His  
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Cys Leu Pro Ala Lys Phe Thr Thr Met His Leu Pro Leu Asn Cys Thr  
210 215 220

Glu Leu Ser Ser Val Ile Lys Val Val Met Leu Val Glu Glu Cys Gln  
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Cys Lys Val Lys Thr Glu His Glu Asp Gly His Ile Leu His Ala Gly  
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Ser Gln Asp Ser Phe Ile Pro Gly Val Ser Ala  
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<223> TKc; Region: Serine/Threonine protein kinases, catalytic domain

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<301> ten Dijke, P., Yamashita, H., Ichijo, H., Franzen, P., Laiho, M., Miyazono, K., and Heldin, C.H.  
<302> Characterization of type I receptors for transforming growth factor-beta and activin  
<303> Science  
<304> 264  
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<306> 101-104  
<307> 1994  
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<309> 2000-10-31  
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<301> Ide, H., Katoh, M., Sasaki, H., Yoshida, T., Aoki, K., Nawa, Y., Osada, Y., Sugimura, T., and Terada, M.  
 <302> Cloning of human bone morphogenetic protein type IB receptor (BMPR-IB) and its expression in prostate cancer in comparison with other BMPRs  
 <303> Oncogene  
 <304> 14  
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 <306> 1377-1382  
 <307> 1997  
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<300>  
 <301> Ide, H., Saito-Ohara, P., Ohnami, S., Osada, Y., Ikeuchi, T., Yoshida, T., and Terada, M.  
 <302> Assignment of the BMPR1A and BMPR1B genes to human chromosome 10q22.3 and 4q23-->q24 by in situ hybridization and radiation hybrid mapping  
 <303> Cytogenet. Cell. Genet.  
 <304> 81  
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 <306> 285-286  
 <307> 1998  
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<300>  
 <301> Astrom, A.K., Jin, D., Imamura, T., Roijer, E., Rosenzweig, B., Miyazono, K., ten Dijke, P., and Stenman, G.  
 <302> Chromosomal localization of three human genes encoding bone morphogenetic protein receptors  
 <303> Mamm. Genome  
 <304> 10  
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 Thr Pro Arg Pro Lys Val Leu Arg Cys Lys Cys His His His Cys Pro  
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Leu Asp Ala Lys Ser Met Leu Lys Leu Ala Tyr Ser Ser Val Ser Gly	
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Leu Cys His Leu His Thr Glu Ile Phe Ser Thr Gln Gly Lys Pro Ala	
315 320 325	
att gcc cat cga gat ctg aaa agt aaa aac att ctg gtg aag aaa aat	1302
Ile Ala His Arg Asp Leu Lys Ser Lys Asn Ile Leu Val Lys Lys Asn	
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Gly Thr Cys Cys Ile Ala Asp Leu Gly Leu Ala Val Lys Phe Ile Ser	
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Asp Thr Asn Glu Val Asp Ile Pro Pro Asn Thr Arg Val Gly Thr Lys	
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Arg Tyr Met Pro Pro Glu Val Leu Asp Glu Ser Leu Asn Arg Asn His	
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Gln Leu Pro Tyr His Asp Leu Val Pro Ser Asp Pro Ser Tyr Glu Asp	
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Met Arg Glu Ile Val Cys Ile Lys Lys Leu Arg Pro Ser Phe Pro Asn	
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Glu Cys Trp Ala His Asn Pro Ala Ser Arg Leu Thr Ala Leu Arg Val	
475 480 485	
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Lys Lys Thr Leu Ala Lys Met Ser Glu Ser Gln Asp Ile Lys Leu	
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35 40 45

Thr Asp Gly Tyr Cys Phe Thr Met Ile Glu Glu Asp Asp Ser Gly Leu  
50 55 60

Pro Val Val Thr Ser Gly Cys Leu Gly Leu Glu Gly Ser Asp Phe Gln  
65 70 75 80

Cys Arg Asp Thr Pro Ile Pro His Gln Arg Arg Ser Ile Glu Cys Cys  
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Thr Glu Arg Asn Glu Cys Asn Lys Asp Leu His Pro Thr Leu Pro Pro  
100 105 110

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Arg Asp Leu Ile Glu Gln Ser Gln Ser Ser Gly Ser Gly Ser Gly Leu  
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Pro Leu Leu Val Gln Arg Thr Ile Ala Lys Gln Ile Gln Met Val Lys  
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Gln Ile Gly Lys Gly Arg Tyr Gly Glu Val Trp Met Gly Lys Trp Arg  
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Asn Ile Leu Gly Phe Ile Ala Ala Asp Ile Lys Gly Thr Gly Ser Trp  
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Thr Gln Leu Tyr Leu Ile Thr Asp Tyr His Glu Asn Gly Ser Leu Tyr  
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Ser Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Lys  
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360

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Gln Met Gly Lys Leu Met Thr Glu Cys Trp Ala His Asn Pro Ala Ser  
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